

27 (new). A biased combinatorial gene expression library, comprising a pool of expression constructs, each expression construct containing cDNA or genomic DNA fragments some of which are preselected from a plurality of species of donor organisms for comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in secondary metabolism, in which the cDNA or genomic fragments are operably associated with one or more regulatory regions that drive expression of genes encoded by the cDNA or genomic DNA fragments in an appropriate host organism.

28 (new). A biased combinatorial gene expression library, comprising a pool of expression constructs, each expression construct containing cDNA or genomic DNA fragments some of which are preselected from a plurality of species of donor organisms by hybridization of the cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in secondary metabolism, in which the cDNA or genomic fragments are operably associated with one or more regulatory regions that drive expression of genes encoded by the cDNA or genomic DNA fragments in an appropriate host organism.

29 (new). The biased combinatorial gene expression library of claim 27 wherein some of the cDNA or genomic fragments are preselected by hybridization of the cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in polyketide biosynthesis, peptide biosynthesis, glycoside biosynthesis, aminoglycoside biosynthesis, mevalonic acid biosynthesis, or glucose transfer systems.

30 (new). The biased combinatorial gene expression library of claim 28 wherein some of the cDNA or genomic fragments are preselected by hybridization of the cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in polyketide biosynthesis, peptide biosynthesis, glycoside biosynthesis, aminoglycoside biosynthesis, mevalonic acid biosynthesis, or glucose transfer systems.

31 (new). The biased combinatorial gene expression library of claim 27 wherein some of the cDNA or genomic fragments are preselected by hybridization of the cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in antibiotic biosynthesis.

32 (new). The biased combinatorial gene expression library of claim 28 wherein some of the cDNA or genomic fragments are preselected by hybridization of the cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in antibiotic biosynthesis.

33 (new). The biased combinatorial gene expression library of claim 27 wherein some of the cDNA or genomic fragments are preselected by hybridization of the cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in the biosynthesis of beta-lactams, macrolides, alkaloids, bryostatins, carotenoids, steroids, or retinoids.

34 (new). The biased combinatorial gene expression library of claim 28 wherein some of the cDNA or genomic fragments are preselected by hybridization of the cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in the biosynthesis of beta-lactams, macrolides, alkaloids, bryostatins, carotenoids, steroids, or retinoids.

35 (new). The biased combinatorial gene expression library of claim 27 wherein some of the cDNA or genomic fragments are preselected by hybridization of the cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in the biosynthesis of actinorhodin, thiostrepton, virginiamycin, valinomycin, actinomycin, tetracycline, oxytetracycline, puromycin, doxorubicin, taxol, chloramphenicol, nalidixic acid, mithramycin, novobiocin, vulpinic acid, usnic acid, kainic acid, podophyllotoxin, brevitoxin, camptothecin, or artemisinin.

36 (new). The biased combinatorial gene expression library of claim 28 wherein some of the cDNA or genomic fragments are preselected by hybridization of the

cDNA or genomic fragments to nucleic acid probes comprising nucleotide sequences that encode for proteins or fragments thereof that are involved in the biosynthesis of actinorhodin, thiostrepton, virginiamycin, valinomycin, actinomycin, tetracycline, oxytetracycline, puromycin, doxorubicin, taxol, chloramphenicol, nalidixic acid, mithramycin, novobiocin, vulpinic acid, usnic acid, kainic acid, podophyllotoxin, brevitoxin, camptothecin, or artemisinin.

37 (new). The biased combinatorial gene expression library of claim 27 wherein the plurality of species of donor organisms from which the cDNA or genomic DNA fragments are preselected, are from an environmental sample.

38 (new). The biased combinatorial gene expression library of claim 28 wherein the plurality of species of donor organisms from which the cDNA or genomic DNA fragments are preselected, are from an environmental sample.

39 (new). The biased combinatorial gene expression library of claim 27 wherein the environmental sample is from soil, deposits near hot springs, deposits near thermal vents, freshwater filtrates, marine sediments, estuarine sediments, or seawater filtrates.

40 (new). The biased combinatorial gene expression library of claim 28 wherein the environmental sample is from soil, deposits near hot springs, deposits near thermal vents, freshwater filtrates, marine sediments, estuarine sediments, or seawater filtrates.

41 (new). The biased combinatorial gene expression library of claim 27 wherein the expression constructs are contained in host cells.

42 (new). The biased combinatorial gene expression library of claim 28 wherein the expression constructs are contained in host cells.